



Comparison of genomic reliability in national genomic evaluation of dairy cattle populations

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INTRODUCTION

GENOMIC EVALUATIONS → Short history vs CONVENTIONAL EV.

Meuwissen et al., 2001

Daughter-Dam Comparison, the '20s

No standardized method

Different countries:

- Different methodologies adopted
- Collecting and handling of genomic data
 - Calculating genomic reliability



AIM OF THE STUDY

ANALYZE AND COMPARE NATIONAL GENOMIC EVALUATIONS
(RELIABILITIES)



1. Numerical data analysis

Member countries



ITBC Data Exchange Area (*IDEA*) database



Check and
Validation



MACE

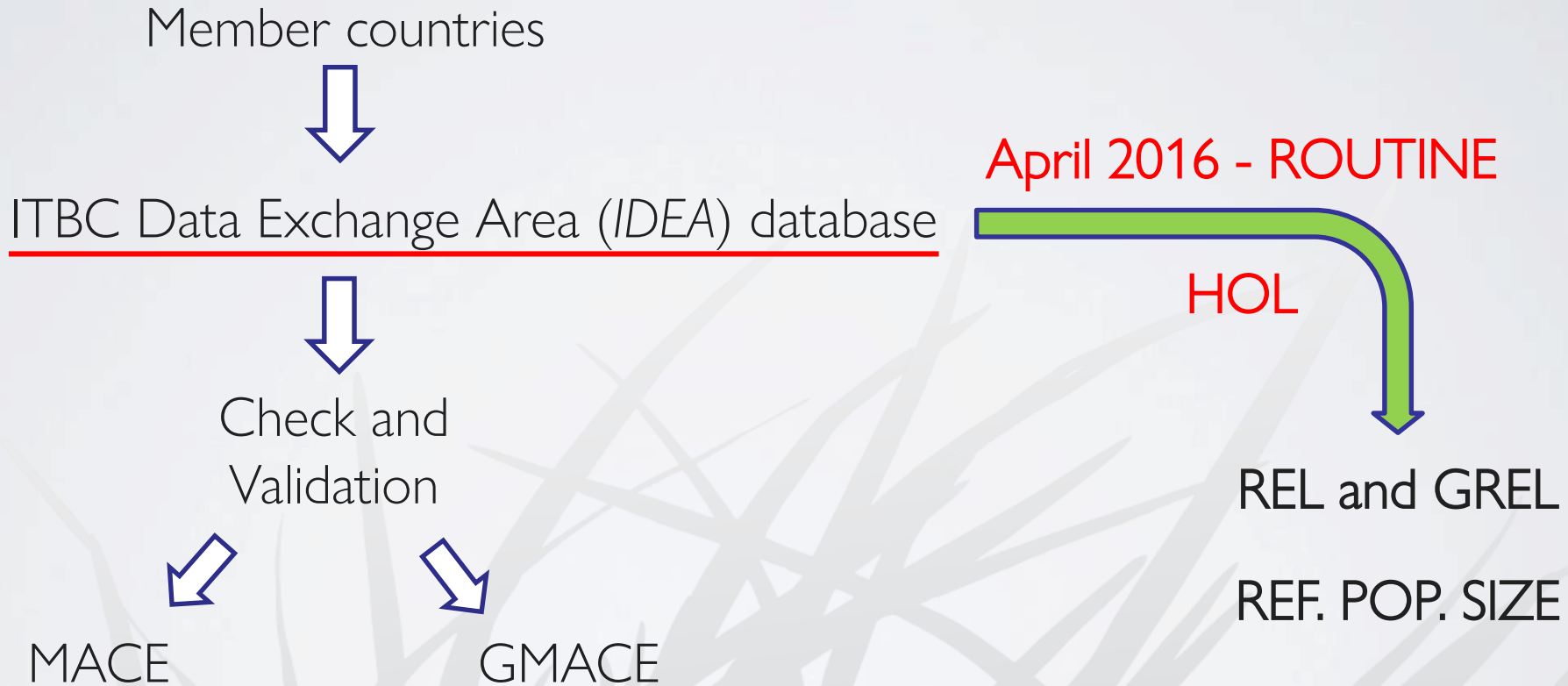


GMACE



MATERIALS AND METHODS

1. Numerical data analysis



2. Statistical analysis on collected data



MATERIALS AND METHODS

2. Statistical analysis on collected data

μ, σ, obs

Linear regression

$$\text{GAIN}_{\text{REL}} = b \cdot (\text{ref. pop.})$$

GAIN_{REL} { $\text{GREL} - \text{REL}$ \Rightarrow Bull submitted both for MACE and GMACE

All dataset

Within POP (all traits evaluated)

Within TRA (all participating populations)



MATERIALS AND METHODS

Bull submitted both for MACE and GMACE

“transition bulls” and “old bulls”

11 POP (EBVs + GEBVs) X 38 TRAIT(S)

Populations - trait combinations available: 339 (418 possible)

POP – TRA	GMACE	GREL + REL	%
POP7 – mil	65.934	8.334	12,64
POP4 – msb	48.917	114	0,23
POP4 – cc2	48.998	276	0,56

How countries send data to ITBC?



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BETTER DATASET for Statistical Analysis



ALL BULLS SUBMITTED FOR GMACE



MATERIALS AND METHODS

ALL BULLS SUBMITTED FOR GMACE

$$\text{GAIN}_{\text{REL}} = \text{GREL} - \text{PArel} \longrightarrow \text{PArel} = 0.25 \cdot (\text{Sire}_{\text{rel}} + \text{Dam}_{\text{rel}})$$

339 combinations available:

17.792.724 records (GMACE)

75,91%

UNKNOWN PARENTS

13.507.057

KNOWN PARENTS

4.285.667 (24,09%)

21,42%

WITHOUT PARENTS REL

917.800

78,58%

WITH KNOWN PARENTS & PARENTS REL

3.367.867 records (18,93%)



MATERIALS AND METHODS

2. Statistical analysis on collected data

μ, σ, obs

Linear regression

$$\text{GAIN}_{\text{REL}} = b \cdot (\text{ref. pop.})$$

GAIN_{REL} {
GREL - REL \Rightarrow Bull submitted both for MACE and GMACE
GREL - PArel \Rightarrow **All bulls submitted for GMACE**

All dataset

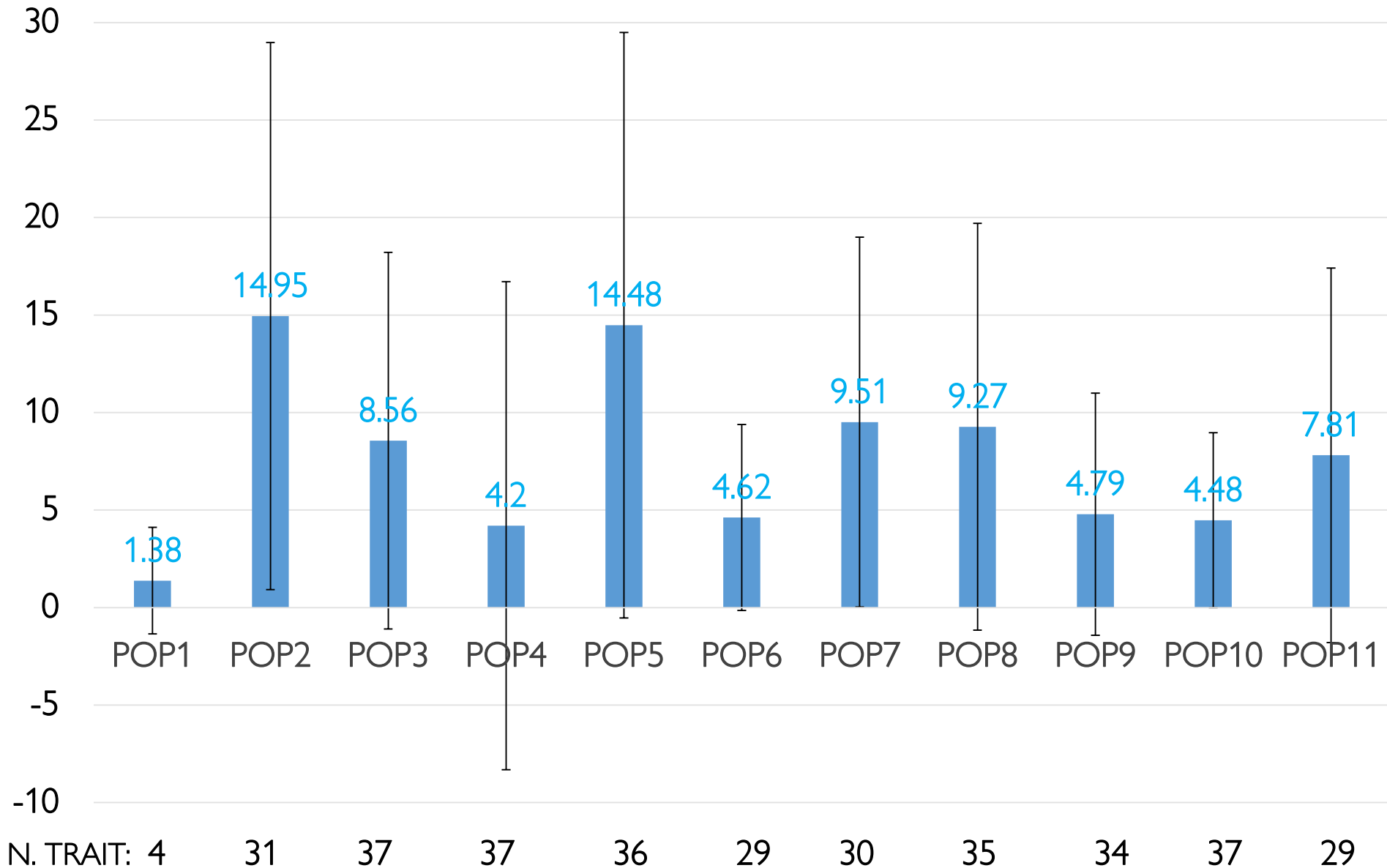
Within POP (all traits evaluated)

Within TRA (all participating populations)



$$\text{GAIN}_{\text{REL}} = \text{GREL} - \text{REL}$$

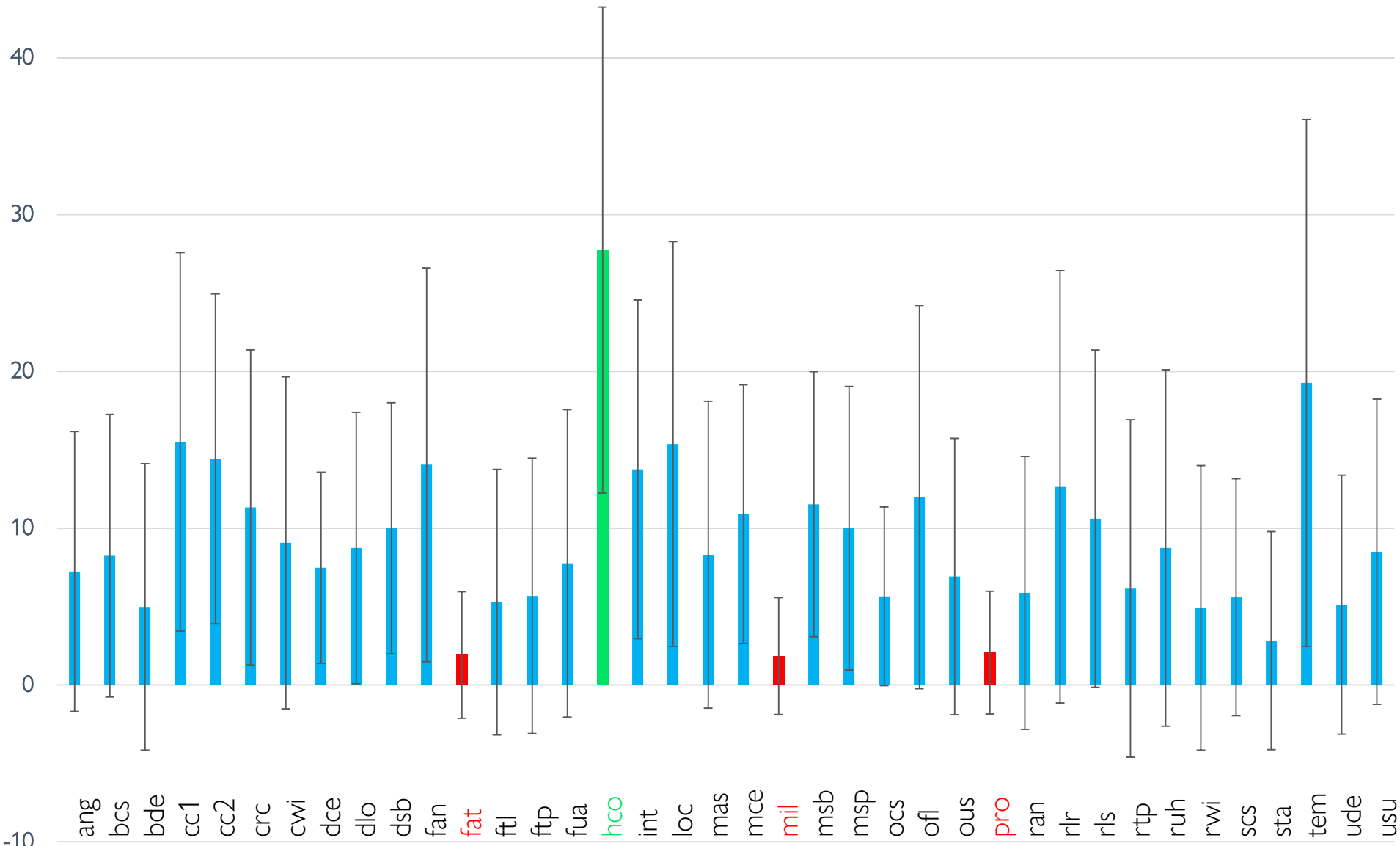
WITHIN POPULATIONS (ALL TRAITS EVALUATED)





$$\text{GAIN}_{\text{REL}} = \text{GREL} - \text{REL}$$

WITHIN TRAIT (ALL PARTECIPATING POPULATIONS)





$$\text{GAIN}_{\text{REL}} = \text{GREL} - \text{REL}$$

Linear Regression: $\text{GAIN}_{\text{REL}} = b \cdot (\text{ref.pop.})$

POP	SLOPE (b) E-04	SE (b) E-05	<i>p-value</i>	R ²	SE	n. traits
ALL	2.81	1.98	0.000	37.3	9.07	338
POP1	4.38	6.26	0.020	94.2	0.39	4
POP2	63.45	60.29	0.000	78.7	7.96	31
POP3	3.05	3.92	0.000	62.8	6.25	37
POP4	0.67	4.42	0.137	6.2	8.22	36
POP5	4.78	4.51	0.000	76.3	8.05	36
POP6	1.58	2.01	0.000	68.7	3.23	29
POP7	3.35	4.68	0.000	63.9	7.22	30
POP8	5.86	5.94	0.000	74.1	8.32	35
POP9	2.02	2.75	0.000	62.1	3.69	34
POP10	1.54	1.3	0.000	79.5	2.25	37
POP11	28.92	48.97	0.000	55.5	7.16	29



$$\text{GAIN}_{\text{REL}} = \text{GREL} - \text{REL}$$

Linear Regression: $\text{GAIN}_{\text{REL}} = b \cdot (\text{ref.pop.})$

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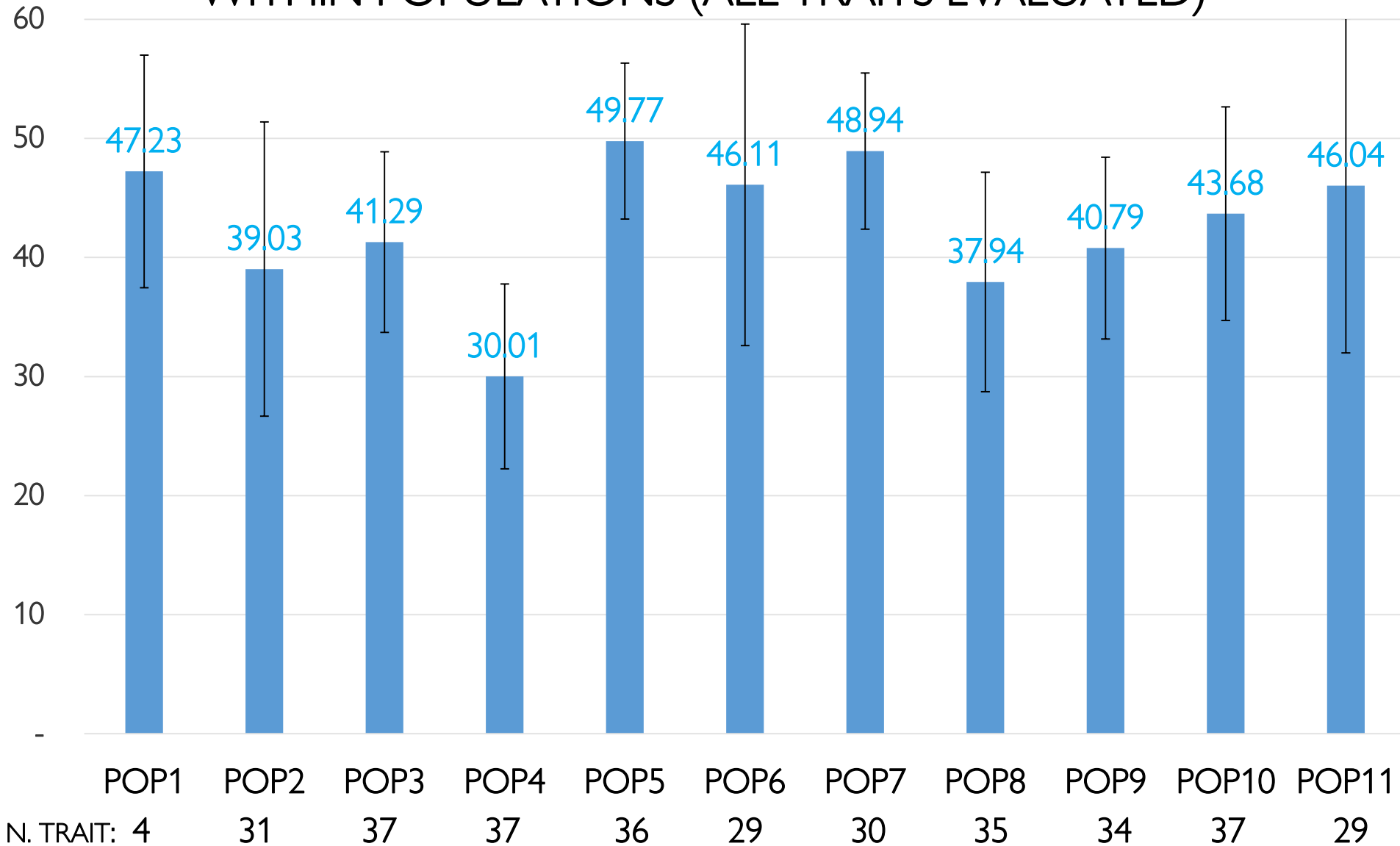
TRA	SLOPE (b) E-04	SE (b) E-05	<i>p-value</i>	R ²	SE	n. COU
cc1	5.36	17.06	0.026	62.2	11.48	7
cc2	5.30	14.48	0.008	62.6	10.96	9
dce	2.91	5.94	0.004	80.0	3.80	7
fat	0.55	4.23	0.229	14.3	3.54	11
mil	0.57	3.64	0.153	19.6	3.05	11
pro	0.58	4.02	0.184	17.1	3.37	11



$$\text{GAIN}_{\text{REL}} = \text{GREL} - \text{PArel}$$

All bulls submitted for GMACE

WITHIN POPULATIONS (ALL TRAITS EVALUATED)



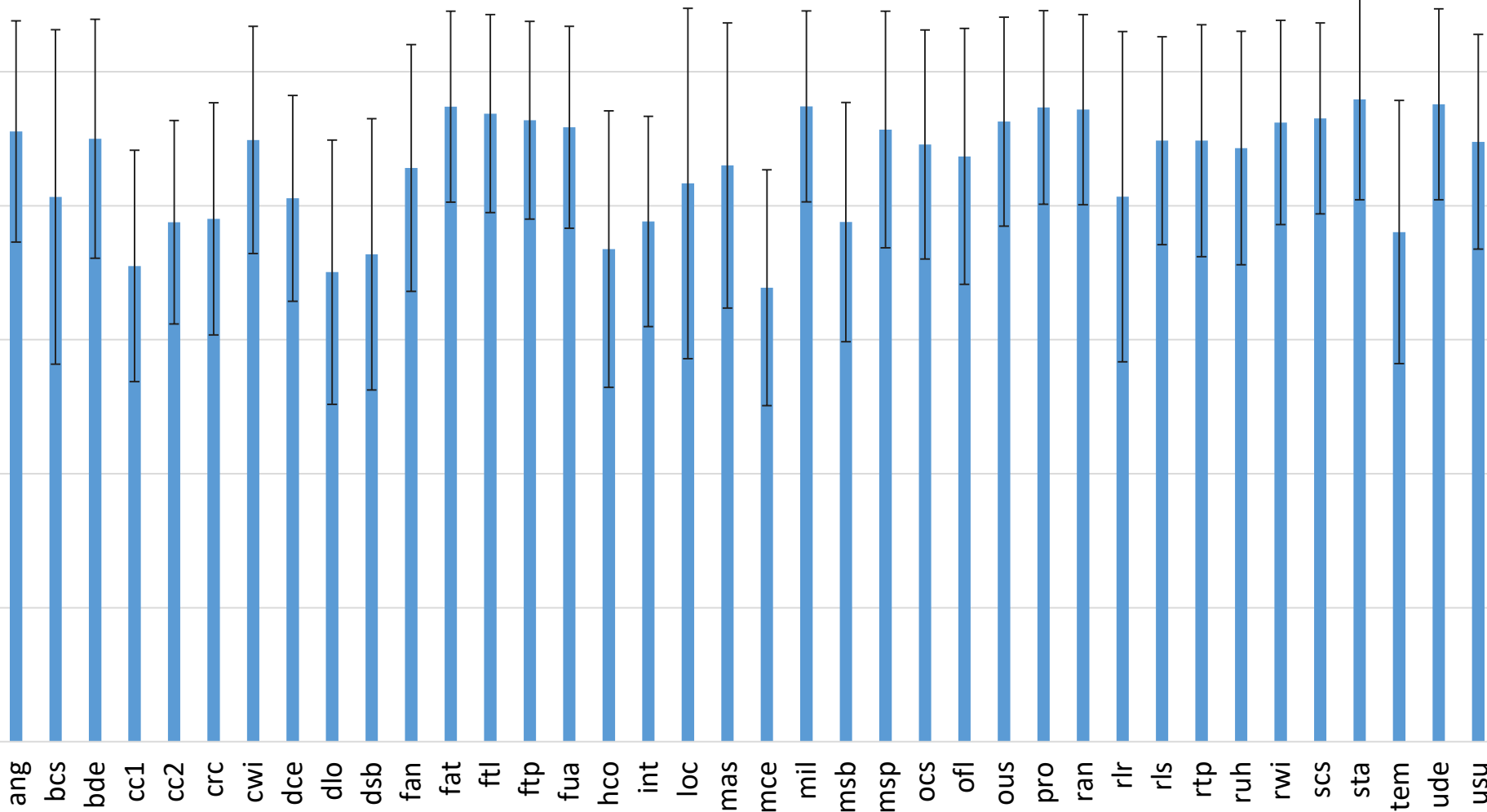


$$\text{GAIN}_{\text{REL}} = \text{GREL} - \text{PArel}$$

All bulls submitted for GMACE

WITHIN TRAITS (ALL PARTECIPATING POPULATIONS)

60



0

10

20

30

40

50

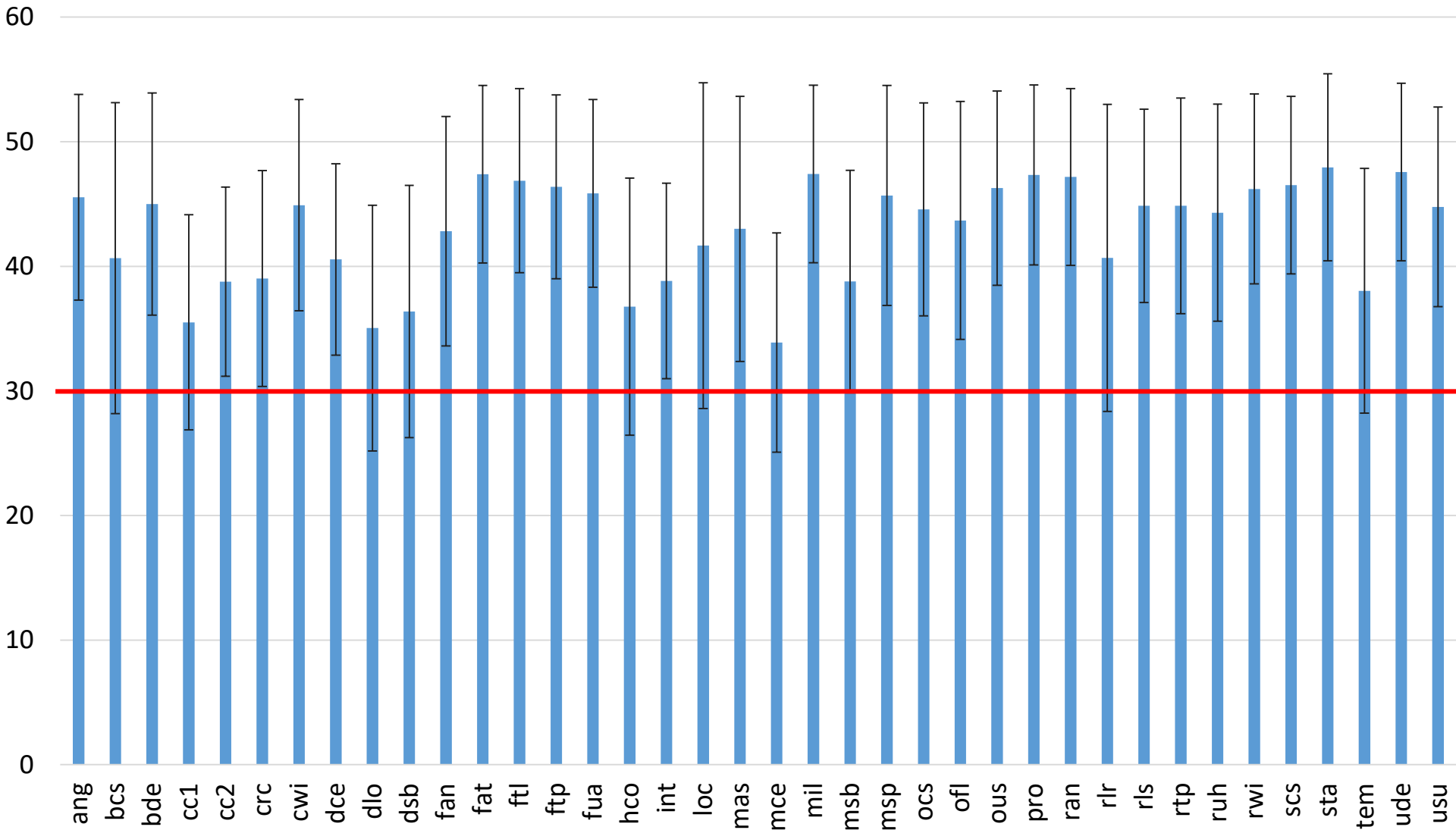
60



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All bulls submitted for GMACE

WITHIN TRAITS (ALL PARTECIPATING POPULATIONS)





$$\text{GAIN}_{\text{REL}} = \text{GREL} - \text{PArel}$$

Linear Regression: $\text{GAIN}_{\text{REL}} = b \cdot (\text{ref.pop.})$

WITHIN POPULATIONS: $p\text{-value} < 0.01$ | \downarrow SE (b) | \uparrow R² | \uparrow SE

	SLOPE (b)	R ²	SE
MIN	0.0010 POP4	94.4 POP8	9.09 POP8
MAX	0.0169 POP11	99.8 POP1	2.49 POP1

WITHIN TRAITS: $p\text{-value} < 0.01$ | + (b) | \downarrow SE (b) | \uparrow R² | \uparrow SE

High REL and small REF POP size



CONCLUSIONS

Different methods used make comparisons difficult

Results show difference between countries

MARGINAL INCREASE IN REL:

1% GREL – PArel	\propto	100	→	1'000 bulls
1% GREL – REL	\propto	1'000	→	10'000 bulls

Heritability and Genotypes



CONCLUSIONS

Further analysis:

Study the relationship between $GAIN_{rel}$ and h^2

Test if EBV_{rel} of ref. pop. bulls can be related to h^2 of traits and also on $GEBV_{rel}$

Countries have shown interest in new solutions: more homogeneous methods may be necessary

G_{REL} WG



PERSONAL ACKNOWLEDGMENTS

Zengting Liu, vit



Interbull Centre





THANKS FOR YOUR
ATTENTION